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APPLICATION NUMBER	FILING DATE	GRP ART UNIT	FIL FEE REC'D	ATTY. DOCKET NO	DRAWINGS	TOT CLAIMS	IND CLAIMS
09/965,654	09/27/2001	2152	0.00	IPT-00601	2	31	2

CONFIRMATION NO. 3485

Patent Group
Foley, Hoag & Eliot LLP
One Post Office Square
Boston, MA 02109-2170

FILING RECEIPT

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Date Mailed: 10/22/2001

Receipt is acknowledged of this nonprovisional Patent Application. It will be considered in its order and you will be notified as to the results of the examination. Be sure to provide the U.S. APPLICATION NUMBER, FILING DATE, NAME OF APPLICANT, and TITLE OF INVENTION when inquiring about this application. Fees transmitted by check or draft are subject to collection. Please verify the accuracy of the data presented on this receipt. If an error is noted on this Filing Receipt, please write to the Office of Initial Patent Examination's Customer Service Center. Please provide a copy of this Filing Receipt with the changes noted thereon. If you received a "Notice to File Missing Parts" for this application, please submit any corrections to this Filing Receipt with your reply to the Notice. When the USPTO processes the reply to the Notice, the USPTO will generate another Filing Receipt incorporating the requested corrections (if appropriate).

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Domestic Priority data as claimed by applicant

Foreign Applications

If Required, Foreign Filing License Granted 10/20/2001

Projected Publication Date: To Be Determined - pending completion of Missing Parts

Non-Publication Request: No

Early Publication Request: No

** SMALL ENTITY **

Title

Protein data analysis

Preliminary Class

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OCT 24 2001

PATENT DEPT.
DOCKETING



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ATTORNEYS AT LAW

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Date: January 28, 2002

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Client Matter#: 23298-601

From: Robert A. Greenberg

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Message

Re: U.S. Patent Application No. 09/965,654

Title: Protein Data Analysis

Filed: September 27, 2001

Our Reference: IPT-006.01 (23298-00601)

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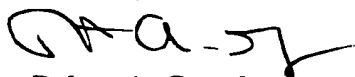
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Dear Sir or Madam:

Enclosed are the following with respect to the above-referenced application:

1. Request for Correction of Filing Receipt/Certificate of Facsimile Transmission; (1 page);
2. Filing Receipt (1 page);
3. First page of Application (1 page); and
4. this Facsimile Cover Page.

Sincerely,


Robert A. Greenberg

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the application of: Edwards et al.

Serial No.: 09/965,654

Filed: September 27, 2001

For: Protein Data Analysis

Attorney Docket No.: IPT-00601

Group Art Unit: 2152

Examiner:

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Attn: Office of Initial Patent Examinations' Customer Service Center

REQUEST FOR CORRECTION OF FILING RECEIPT

Please make the following correction in the formal Filing Receipt, a copy of which is enclosed, for the above-identified patent application.

The Domestic Priority data as claimed by applicant should include a claim of priority to U.S. Application Serial No. 09/671,817, filed on September 27, 2000. This information appears in the first sentence of the first page of the originally submitted patent application.

Should there be any questions concerning this request, the Examiner is invited to contact the undersigned at (617) 832-1291.


I hereby certify that this correspondence is being facsimile transmitted to the Patent and Trademark Office on:

1/28/02

Date

Leresa Bauld

Respectfully submitted,
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Dated: January 28, 2001

Attorney Docket: IPT-00601

PROTEIN DATA ANALYSIS

Reference to Related Applications

This application claims priority to co-pending U.S. Application Serial No. 09/671,817, filed on September 27, 2000, entitled "Methods for Determining the Biochemical and Biophysical Properties of Proteins". This application is incorporated by reference in its entirety herein.

Background

Genome sequencing projects are providing vast amounts of information. With the whole genome of many organisms, including humans, complete or nearing completion, the next challenge involves the characterization of these gene products, proteins. This flood of sequence information, coupled with recent advances, in molecular and structural biology have also lead to the concept of "structural proteomics" or "structural genomics", the determination of three dimensional (3D) protein structures on a genome-wide scale. The 3D-structural information of proteins may be used to uncover clues to protein function difficult to detect from sequence analysis. This application of structural proteomics is, in part, driven by the realization that fewer than 30% of all predicted eukaryotic proteins have a known function.

While useful, analysis of the DNA sequence alone generally does not allow one to infer the structure or function of gene products unless the sequence has high homology to another gene of known function. Gene sequence information alone often does not provide a complete and accurate profile of protein function or structure. After transcription from DNA to RNA, the mRNA transcript may be spliced in different ways prior to translation into the protein. Following translation, many proteins are modified, for example, by the addition of one or more